AMENDMENTS TO THE SPECIFICATION:

Please amend the substituted specification filed February 22, 2008 as follows:

Please delete the paragraph spanning lines 7-9 of page 29 of the substitute specification filed February 22, 2008, and insert the following therefor:

The sequence of the compound peptide in the one-letter notation is Ac-F-I-E-G-R-A-D-S-K-S-S-COOH (SEQ ID NO:2) has an acetylated free α-NH_2-terminus and a free COOH-terminus. According to our "SLA"-definitions, we distinguish the following functions:

Please delete the paragraph spanning lines 20-24 of page 29 of the substitute specification filed February 22, 2008, and insert the following therefor:

The factor Xa-restriction cleavage site, forms the "A"-part of the compound and is spatially separated from the "S-L"-part. When released by cleavage, the hydrophobic Ac-F-I-E-G-R (SEQ ID NO:1) cargo will separate, leaving a more hydrophilic compound still attached to its target peptide. In the secondary run (run 2), this more hydrophilic peptide will shift in front of the bulk of unmodified peptides. See Figure 7.

Please delete the paragraphs spanning lines 1-7 of page 30 of the substitute specification filed February 22, 2008, and insert the following therefor:

For instance, the molecule could be composed of the caspase-1 inhibitory peptide aldehyde Ac-YVAD-CHO (SEQ ID NO:4), elongated versus the N-terminal side by, a short peptide carrying the factor X_a restriction cleavage site, for instance:

Ac-A-A-I-E-G-R-Y-V-A-D-CHO (SEQ ID NO:3). While the Y-V-A-D-sequence will direct the molecule to the active site of the caspase-1 type proteases ("S"-group) the COOH-terminus converted into an aldehyde will create the cross-link ("L"-group). The NH_2-terminal part of the molecule can be cleaved off by using factor X_a. See Figure 9.

Please delete the paragraphs spanning lines 15-24 of page 33 of the substitute specification filed February 22, 2008, and insert the following therefor:

Peptide elution was as in Figure 1A. The peptide elution profile of pooled fraction D, containing the primary fractions 4-9-14-19-24 is shown in Fig. 3A. We observe peaks emerging from the intervals 9 and 14. Peak 9* eluting in front of interval 9 could not be identified as a peptide. Peak 9**, eluting on the tailing side of interval 9 is derived from the excess of CP which did not react with actin. It is the NH_2-terminal part of CP with sequence Ac-Phe-Ile-Glu-Glu-Arg (SEQ ID NO:8). This was confirmed by mass spectrometry.

From interval 14 there is a new peak emerging in front of the bulk of unmodified peptides (shown in black). This peak was identified as the cross-linked peptide

ADSKSS (SEQ ID NO:5)
|
19 actin 50